

c 9/748,710.

Set Name Query

side by side

Hit Count Set Name

result set

DB=USPT,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ

<u>L16</u>	l14 and exon	0	<u>L16</u>
<u>L15</u>	L14 and bamh1	0	<u>L15</u>
<u>L14</u>	5866330.pn.	2	<u>L14</u>
<u>L13</u>	l11 and exon	1	<u>L13</u>
<u>L12</u>	L11 and bamH1	0	<u>L12</u>
<u>L11</u>	L10 and (serial analysis near5 gene expression\$1)	2	<u>L11</u>
<u>L10</u>	(one base anchor\$2 or single base anchor\$2) near5 primer\$1	12	<u>L10</u>
<u>L9</u>	l7 and exon	0	<u>L9</u>
<u>L8</u>	l7 and (one base anchor\$2 or single base anchor\$2)	0	<u>L8</u>
<u>L7</u>	L5 and ((restrict\$3 or recognit\$3) near5 BamH1)	1	<u>L7</u>
<u>L6</u>	L5 and ((recognition sequence or restrict\$3) near5 end\$1 near5 BAmH1)	0	<u>L6</u>
<u>L5</u>	serial analysis near5 gene expression	142	<u>L5</u>
<u>L4</u>	sage tag41	0	<u>L4</u>
<u>L3</u>	serial analysis of gene expression	0	<u>L3</u>
<u>L2</u>	sage	8162	<u>L2</u>
<u>L1</u>	serial analysis of gene expression	0	<u>L1</u>

END OF SEARCH HISTORY

End of Result Set☐ **Generate Collection**

L7: Entry 1 of 1

File: USPT

Oct 8, 2002

DOCUMENT-IDENTIFIER: US 6461814 B1

TITLE: Method of identifying gene transcription patterns

Brief Summary Text (11):

Recently, a variation of PCR for a random cDNA sequencing approach was described by Velculescu et al. (Velculescu, V. E. et al., Science 270:484 (1995)). This technique, called Serial Analysis of Gene Expression (SAGE), generates short, defined sequences from cDNAs which are randomly ligated in a tail-to-tail fashion and amplified by PCR to form "di-tags". These di-tags are then concatenated into arrays which are cloned and analyzed by DNA sequencing. Because each sequencing template contains identifiable tags corresponding to many genes, the potential throughput of SAGE exceeds traditional cDNA sequencing, allowing gene transcription profiling in many laboratories.

Brief Summary Text (29):

"A 5' cloning restriction endonuclease" as used herein, means a restriction endonuclease having a corresponding methylase or other protection means that can protect any DNA from cleavage by the enzyme. Preferably, the 5' cloning restriction endonuclease recognizes a sequence of between about four to ten bases. Examples of this most preferably, the 5' cloning restriction endonuclease is EcoRI, BamHI, HindIII

Other Reference Publication (49):

Velculescu et al., "Serial Analysis of Gene Expression," Science 270: 484-487, 1995.

09/748, 710

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 12:13:29 ON 19 MAR 2003

=> file caplus medline biosis
COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.21	0.21

FULL ESTIMATED COST

FILE 'CAPLUS' ENTERED AT 12:13:44 ON 19 MAR 2003

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FILE 'MEDLINE' ENTERED AT 12:13:44 ON 19 MAR 2003

FILE 'BIOSIS' ENTERED AT 12:13:44 ON 19 MAR 2003

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=> s serial analysis gene expression#

L1 39 SERIAL ANALYSIS GENE EXPRESSION#

=> s l1 and bamH1 and exon

L2 0 L1 AND BAMH1 AND EXON

=> s l1 and exon

L3 1 L1 AND EXON

=> s l1 and bamH1

L4 0 L1 AND BAMH1

=> d l3 bib ab kwic

L3 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2003 ACS

AN 2000:38520 CAPLUS

DN 132:203734

TI Generation of longer cDNA fragments from serial analysis of gene expression tags for gene identification

AU Chen, Jian-Jun; Rowley, Janet D.; Wang, San Ming

CS Section of Hematology/Oncology, University of Chicago Medical Center, Chicago, IL, 60637, USA

SO Proceedings of the National Academy of Sciences of the United States of America (2000), 97(1), 349-353

CODEN: PNASA6; ISSN: 0027-8424

PB National Academy of Sciences

DT Journal

LA English

AB A technique was developed called the generation of longer cDNA fragments from serial anal. of gene expression (SAGE) tags for gene identification (GLGI), to convert SAGE tags of 10 bases into their corresponding 3' cDNA fragments covering hundred bases. A primer contg. the 10-base SAGE tag is used as the sense primer, and a single base anchored oligo(dT) primer is used as an antisense primer in PCR, together with Pfu DNA polymerase. By using this approach, a cDNA fragment extending from the SAGE tag toward the 3' end of the corresponding sequence can be generated. Application of the GLGI technique can solve 2 crit. issues in applying the SAGE technique: one is that a longer fragment corresponding to a SAGE tag, which has no match in databases, can be generated for further studies; the other is that the specific fragment corresponding to a SAGE tag can be identified from multiple sequences that match the same SAGE tag. The development of the GLGI method provides several potential applications.

First, it provides a strategy for even wider application of the SAGE technique for quant. anal. of global gene expression. Second, a combined application of SAGE/GLGI can be used to complete the catalog of the expressed genes in human and in other eukaryotic species. Third, it can be used to identify the 3' cDNA sequence from any **exon** within a gene. It can also be used to confirm the reality of exons predicted by bioinformatic tools in genomic sequences. Fourth, a combined application of SAGE/GLGI can be applied to define the 3' boundary of expressed genes in the genomic sequences in human and in other eukaryotic genomes.

RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB A technique was developed called the generation of longer cDNA fragments from serial anal. of gene expression (SAGE) tags for gene identification (GLGI), to convert SAGE tags of 10 bases into their corresponding 3' cDNA fragments covering hundred bases. A primer contg. the 10-base SAGE tag is used as the sense primer, and a single base anchored oligo(dT) primer is used as an antisense primer in PCR, together with Pfu DNA polymerase. By using this approach, a cDNA fragment extending from the SAGE tag toward the 3' end of the corresponding sequence can be generated. Application of the GLGI technique can solve 2 crit. issues in applying the SAGE technique: one is that a longer fragment corresponding to a SAGE tag, which has no match in databases, can be generated for further studies; the other is that the specific fragment corresponding to a SAGE tag can be identified from multiple sequences that match the same SAGE tag. The development of the GLGI method provides several potential applications. First, it provides a strategy for even wider application of the SAGE technique for quant. anal. of global gene expression. Second, a combined application of SAGE/GLGI can be used to complete the catalog of the expressed genes in human and in other eukaryotic species. Third, it can be used to identify the 3' cDNA sequence from any **exon** within a gene. It can also be used to confirm the reality of exons predicted by bioinformatic tools in genomic sequences. Fourth, a combined application of SAGE/GLGI can be applied to define the 3' boundary of expressed genes in the genomic sequences in human and in other eukaryotic genomes.

ST cDNA generation SAGE tag gene identification; **serial analysis gene expression** cDNA generation; GLGI cDNA generation **serial analysis gene expression**

=> s pattern# (10a) gene transcription#
L5 369 PATTERN# (10A) GENE TRANSCRIPTION#

=> s l5 and gene expression#
1 FILES SEARCHED...
L6 177 L5 AND GENE EXPRESSION#

=> s l6 and exon#
L7 3 L6 AND EXON#

=> s l7 and BamH1
L8 0 L7 AND BAMH1

=> dup rem l7
PROCESSING COMPLETED FOR L7
L9 2 DUP REM L7 (1 DUPLICATE REMOVED)

=> d l9 1-2 bib ab kwic

L9 ANSWER 1 OF 2 MEDLINE
AN 97211325 MEDLINE
DN 97211325 PubMed ID: 9058323
TI Elements between the protein-coding regions of the adjacent beta 4 and alpha 3 acetylcholine receptor genes direct neuron-specific expression in

the central nervous system.

AU Yang X; Yang F; Fyodorov D; Wang F; McDonough J; Herrup K; Deneris E
CS Department of Neurosciences, Case Western Reserve University School of
Medicine, Cleveland, Ohio 44106-4975, USA.

NC NS18381 (NINDS)
NS29123 (NINDS)

SO JOURNAL OF NEUROBIOLOGY, (1997 Mar) 32 (3) 311-24.
Journal code: 0213640. ISSN: 0022-3034.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 199706

ED Entered STN: 19970620

Last Updated on STN: 19970620

Entered Medline: 19970612

AB The expression patterns of three clustered neuronal nicotinic
acetylcholine receptor (nAChR) subunit genes ordered beta 4, alpha 3, and
alpha 5 overlap extensively in the peripheral nervous system (PNS) but
only partially in the central nervous system (CNS). We have begun to
investigate cell type-specific cis elements regulating these genes by
analyzing in both cell culture and transgenic mice, a 2.8-kb fragment
(-2732/+47) containing the alpha 3 promoter region, the beta 4/alpha 3
intergenic region, and a portion of the beta 4 3'-untranslated
exon. The -2732/+47 fragment is preferentially active in PC12
cells relative to nonneural cell lines. Deletion analysis revealed a cell
type-specific positive transcriptional element positioned in the beta 4
3'-untranslated **exon**. The positive element is likely to be an
enhancer and not a second alpha 3 promoter, because no alpha 3
exons are present in this region. Having shown in cell culture
that cell-type specific cis elements are positioned between the beta 4 and
alpha 3 coding regions, we investigated the activity of -2732/+47 in vivo.
Transgenic mice were generated, which carry the lacZ gene fused downstream
of -2732/+47. Expression of the lacZ transgene is restricted to neurons of
the CNS; no expression was detected in the PNS or in nonneural tissues.
LacZ-positive cells were detected virtually exclusively in a subset of CNS
nuclei that transcribe the endogenous alpha 3 gene. Some overlap was seen
with the beta 4 gene, but nearly none with the alpha 5 gene. Our results
demonstrate that cis elements positioned between the alpha 3 and beta 4
coding regions are important for establishing part of the restricted CNS
patterns of beta 4, alpha 3, and alpha 5 **gene**
transcription.

AB . . . containing the alpha 3 promoter region, the beta 4/alpha 3
intergenic region, and a portion of the beta 4 3'-untranslated
exon. The -2732/+47 fragment is preferentially active in PC12
cells relative to nonneural cell lines. Deletion analysis revealed a cell
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. elements positioned between the alpha 3 and beta 4 coding regions are
important for establishing part of the restricted CNS **patterns**
of beta 4, alpha 3, and alpha 5 **gene transcription**.

CT Check Tags: Animal; Support, U.S. Gov't, P.H.S.

Central Nervous System: CY, cytology

*Central Nervous System: ME, metabolism

Exons

Gene Expression

*Genes

Genes, Reporter

Mice

Mice, Transgenic

*Neurons: ME, metabolism

PC12 Cells
Promoter Regions (Genetics)
Rats
*Receptors, Nicotinic: GE, . . .

L9 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 1
AN 1992:209024 CAPLUS
DN 116:209024
TI K-ras **gene expression** in the regenerating rat liver
AU Park, Sun Hee; Lee, Seung Ki; Park, Jong Sang
CS Coll. Nat. Sci., Seoul Natl. Univ., Seoul, 151-742, S. Korea
SO Han'guk Saenghwa Hakhoechi (1992), 25(1), 9-13
CODEN: KBCJAK; ISSN: 0368-4881
DT Journal
LA Korean
AB K-ras **Gene expression** in the regenerating liver after partial hepatectomy was tested by using dot hybridization. K-ras **Gene transcription** after the partial hepatectomy is amplified and its RNA splicing **pattern** is changed. In normal liver **exon 4a** is spliced out and only K-ras proteins contg. **exon 4b** are produced. In regenerating liver **exon 4b** is spliced out and K-ras proteins contg. **exon 4a** may be formed at a frequency 1000%-fold that in normal liver.
TI K-ras **gene expression** in the regenerating rat liver
AB K-ras **Gene expression** in the regenerating liver after partial hepatectomy was tested by using dot hybridization. K-ras **Gene transcription** after the partial hepatectomy is amplified and its RNA splicing **pattern** is changed. In normal liver **exon 4a** is spliced out and only K-ras proteins contg. **exon 4b** are produced. In regenerating liver **exon 4b** is spliced out and K-ras proteins contg. **exon 4a** may be formed at a frequency 1000%-fold that in normal liver.
ST rat regenerating liver gene Kras transcription; **exon Kras** protein regenerating rat liver
IT Ribonucleic acids, messenger
RL: BIOL (Biological study)
(for gene K-ras protein, in regenerating rat liver, **exon 4a** in)
IT Transcription, genetic
(of gene K-ras, in regenerating rat liver, **exon 4a** in relation to)
IT Rat
(regenerating liver of, gene K-ras transcription in, **exon 4a** in relation to)
IT Liver, metabolism
(regenerating, of rat, gene K-ras transcription in, **exon 4a** in relation to)
IT Genetic element
RL: BIOL (Biological study)
(**exon, 4a**, in gene K-ras mRNA, in regenerating rat liver, **exon 4b** splicing in relation to)
IT G proteins (guanine nucleotide-binding proteins)
RL: BIOL (Biological study)
(p21v-Ki-ras, in regenerating rat liver, **exon 4a** in mRNA for)
IT Gene, animal
RL: BIOL (Biological study)
(c-Ki-ras, transcription of, in regenerating rat liver, **exon 4a** in relation to)

=> s hodgkin cell#
L10 393 HODGKIN CELL#

=>

=> d 110 393 kwic

L10 ANSWER 393 OF 393 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
IT Miscellaneous Descriptors
ABSTRACT HUMAN MALIGNANT LYMPHOMA **HODGKIN CELLS**
STEINBERGS GIANT CELLS

=> d 110 1 kwic

L10 ANSWER 1 OF 393 CAPLUS COPYRIGHT 2003 ACS
IT Hodgkin's disease
(**Hodgkin cell**; loss of B-lineage-specific gene
expression program in Hodgkin and Reed-Sternberg cells of Hodgkin's
lymphoma)

=>